maximum fluorescence (MF) was reached with biotinylated reference peptide without competitor peptide and set to 0% inhibition. The IC50 was determined as half-maximum fluorescence (MF/2 = IC50). Conditions without reference peptide were set to 100% inhibition. This allowed calculation of percentage of binding inhibition using the formula: {1 - (MF competitor peptide - MF no peptide) / (MF reference peptide - MF no peptide)} x 100%. Moreover, T2-A3 cells were tested with the biotinylated influenza A nuclear protein-derived peptide NP265 as reference peptide.--

Please amend the paragraph beginning on page 70, line 17 as follows:

--A computer-assisted peptide-binding prediction program is available on the Internet (~~http://~~bimas.dcrt.nih.gov:80/cgi- bin/molbio/ken_parker comboform), which, for a given allele, scores candidate peptides for their estimated dissociation half life (in minutes). Numerous hTERT-derived 9mers and 10mers are predicted to bind to HLA- A*0201, and these peptides represent candidate CTL epitopes with high affinity for this allele (Table 2). Furthermore, this type of analysis also predicts binding of several other hTERT-derived peptides to non-HLA- A*0201 alleles (Table 3). It has become evident that the threshold of scores that predict binding varies for each HLA allele and will be determined by analyzing scores of peptides previously shown to bind (i.e., "positive controls" in Tables 2 and 3). For example, scores above 500 predict high-affinity binding to HLA-A*0201 whereas scores above 80 and 90 predict binding to HLA-A3. For each hTERT peptide listed in Tables 2 and 3, initial BLAST searches indicate a unique coding sequence within the currently available genomic database. For any given patient, therefore, it is possible to assemble a panel of hTERT peptides, rather than a single epitope potentially prone to mutation, suitable for targeting in immunotherapeutic approaches.--

Please replace the pending sequence listing with the enclosed sequence listing.

REMARKS

Applicants submit herewith a substitute computer readable form (CFR) copy of the "Sequence Listing"; a substitute paper copy of the "Sequence Listing"; and a statement that the content of the paper and computer readable copies are the same and include no new matter, in

compliance with 37 C.F.R. §§ 1.821-1.825. The specification has been amended to correct SEQ ID NOs and correct the sequence listing. No new matter is added.

The Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 20363-015NATL. Should any questions or issues arise concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

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